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RAW SEQUENCE LISTING                    DATE: 01/19/2002
PATENT APPLICATION:   US/10/037,633     TIME: 11:58:24

Input Set : A:\DKGR-SEQS.ST25.txt
Output Set: N:\CRF3\01182002\J037633.raw

**ENTERED**

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   3  <110> APPLICANT: BLABER, MICHAEL
   4         SANLI, GULSAH
   5         BLABER, SACHIKO
   7  <120> TITLE OF INVENTION: SYNTHETIC GENES FOR 2,5-DIKETO-D-GLUCONIC ACID REDUCTASES
   9  <130> FILE REFERENCE: 22201
C-->  11  <140> CURRENT APPLICATION NUMBER: US/10/037,633
C-->  11  <141> CURRENT FILING DATE: 2002-01-03
  11  <150> PRIOR APPLICATION NUMBER: US 60/259527
  12  <151> PRIOR FILING DATE: 2001-01-03
  14  <160> NUMBER OF SEQ ID NOS: 6
  16  <170> SOFTWARE: PatentIn version 3.0
  18  <210> SEQ ID NO: 1
  19  <211> LENGTH: 845
  20  <212> TYPE: DNA
  21  <213> ORGANISM: Corynebacterium species
  23  <220> FEATURE:
  24  <221> NAME/KEY: misc_feature
  25  <223> OTHER INFORMATION: "n" positions designate restriction endonuclease recognition
site
  29  <400> SEQUENCE: 1
W-->  30  nnnatgacag ttcccagcat cgtgctcaac gacggcaatt ccattccccca gctcgggtac      60
  32  ggcgtcttca aggtgccgcc ggcggacacc cagcgcgccg tcgaggaagc gctcgaagtc     120
  34  ggctaccggc acatcgacac cgcggcgatc tacggaaacg aagaaggcgt cggcgccgcg     180
  36  atcgcggcga gcggcatcgc gcgcgacgac ctgttcatca cgacgaagct ctggaacgat     240
  38  cgccacgacg gcgatgagcc cgctgcagcg atcgccgaga gcctcgcgaa gctggcactc     300
  40  gatcaggtcg acctgtacct cgtgcactgg ccgacgcccg ccgccgacaa ctacgtgcac     360
  42  gcgtgggaga agatgatcga gcttcgcgca gccggtctca cccgcagcat cggcgtctcg     420
  44  aaccacctcg tgccgcacct cgagcgcatc gtcgccgcca ccggcgtcgt gccggcggtg     480
  46  aaccagatcg agctgcaccc cgcctaccag cagcgcgaga tcaccgactg ggccgccgcc     540
  48  cagcacgtga agatcgaatc gtggggggcg ctcggtcagg gcaagtacga cctcttcggc     600
  50  gccgagcccg tcactgcggc tgnnnnngn tattattta  nnnnnn nnccgtgctc           660
  52  cgttcgcagc tgcagaaggg tttcgtgatc ttcccgaagt cggtccgccg cgaagccctc     720
  54  nnnnnnnnn naaacttn cga nn nnnnn cgagatcgc cacgatcgac                  780
  56  gcgatggatc cgggcgacgg ttcgggtcgc gtgagcgac accccgatcg agtcgtcgga     840
W-->  58  nnnnn                                                                845
  61  <210> SEQ ID NO: 2
  62  <211> LENGTH: 845
  63  <212> TYPE: DNA
  64  <213> ORGANISM: Corynebacterium species
  66  <400> SEQUENCE: 2
  67  catatgaccg ttccgtctat cgttctgaac gacggtaact ctatcccgca gctgggttac      60
  69  ggtgttttca aagttccgcc ggctgacacc cagcgtgctg ttgaagaagc tctggaagtt     120
  71  ggttaccgtc acatcgacac cgctgctatc tacggcaacg aagaagttgt tggtgctgct     180
  73  atcgctgctt ctggtatcgc tcgtgacgac ctgttcatca ccaccaaact gtggaacgac     240
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 75 cgccacgacg gtgacgaacc ggctgctgct atcgctgaat ctctggctaa actggctctg     300
 77 gatcaggttg acctgtacct ggttcactgg ccgaccccgg ctgctgacaa ctacgttcac     360
 79 gcttgggaaa aaatgatcga actgcgtgct gctggtctga cccgttctat cggtgtttct     420
 81 aaccacctgg ttccgcacct ggaacgtatc gttgctgcta ccggtgttgt tccggctgtt     480
 83 aaccacgatcg aactgcaccc ggcttaccag cagcgtgaaa tcaccgactg ggctgctgct     540
 85 cacgacgtta aaatcgaatc ttggggtccg ctgggtcagg gtaaatacga cctgttcggt     600
 87 gctgaaccgg taaccgctgc tgctgctgct cacggtaaaa ccccggctca ggctgttctg     660
 89 cgttggcacc tgcagaaagg tttcgttgtt ttcccgaaat ctgttcgtcg tgaacgtctg     720
 91 gaagaaaacc tggacgtttt cgacttcgac ctgaccgaca ccgaaatcgc tgctatcgac     780
 93 gctatggatc cggcgacgg ttctggtcgt gtttctgctc accggacga agttgactga     840
 95 agctt                                                                 845
 98 <210> SEQ ID NO: 3
 99 <211> LENGTH: 843
100 <212> TYPE: DNA
101 <213> ORGANISM: Corynebacterium species
103 <220> FEATURE:
104 <221> NAME/KEY: misc_feature
105 <223> OTHER INFORMATION: "n" positions at both ends of sequence represent restriction
endo
106        nuclease recognition sites; "n" positions at residues 49-51, and
107        55-57 represent areas of disagreement in the published sequence f
108        or wild type DKGR-B between Sonoyama and Powers, however, both pu
W--> 109   blished sequences encode the same amino acid
112 <400> SEQUENCE: 3
W--> 113 nnnatgccga acatccccac catcagcctc aacgacggac gccccttcnn ngagnnnggg     60
115 ctcgtcacgt acaacctgcg cggcgacgag ggggtcgcgg ccatggtcgc cgcgatcgac     120
117 tcgggctacc gcctgctcga cacggcggtg aactacgaga acgagagcga ggtcggccga     180
119 gcggtgcgcg cgagcagcgt cgatcgcgac gagctcatcg tggcgagcaa gatcccgggc     240
121 cgccagcacg ggcgcgccga ggcggtcgac agcatccgcg gatcgctcga ccggctgggg     300
123 ctcgacgtga tcgacctgca gctgatccac tggccgaacc ccagcgtggg ccggtggctc     360
125 gacacctggc gcggcatgat cgacgcgcg gaggcgggcc tggtccgctc gatcggcgtc     420
127 tcgaacttca ccgagccgat gctgaagacc ctcatcgacg agaccggggt cacacccgcg     480
129 gtcaaccagg tcgagctcca cccgtacttc cgccaggcgg cgctgcgcgc gttccacgac     540
131 gagcacggca tccgcaccga gagctggagc ccgctcgccc ggcgcagcga gctgctcacc     600
133 gagcagctgc tgcaggagct ggcggtcgtc tacggagtga cgccgacgca ggtggtgctg     660
135 cggtggcacg tgcagctcag cagcacccg atccccaagt ccgccgaccc cgatcgccag     720
137 cgcgagaacg ccgatgtgtt cggcttcgcc ctcaccgccg accaggtcga tgcgatctcg     780
W--> 139 ggcctcgagc gcgggcggct ctgggacggc gaccccgaca cgcacgaaga gatgtagnnn     840
W--> 141 nnn                                                                   843
144 <210> SEQ ID NO: 4
145 <211> LENGTH: 843
146 <212> TYPE: DNA
147 <213> ORGANISM: Corynebacterium species
149 <400> SEQUENCE: 4
150 catatgccga acatcccgac catctctctg aacgacggtc gtccgttccc ggaactgggt     60
152 ctgggtacct acaacctgcg tggtgacgaa ggtgttgctg ctatggttgc tgctatcgac     120
154 tctggttacc gtctgctgga caccgctgtt aactacgaaa acgaatctga agttggtcgt     180
156 gctgttcgtg cttcttctgt tgaccgtgac gaactgatcg ttgctctaa aatcccgggt     240
158 cgtcagcacg gtcgtgctga agctgttgac tctatccgtg ttctctgga ccgtctgggt     300
160 ctggacgtta tcgacctgca gctgatccac tggccgaacc cgtctgttgg tcgttggctg     360
```

```
162  gacacctggc gtggtatgat cgacgctcgt gaagctggtc tggttcgttc tatcggtgtc   420
164  tctaacttca ccgaaccgat gctgaaaacc ctgatcgacg aaaccggtgt tacccccggct  480
166  gttaaccagg ttgaactgca cccgtacttc ccgcaggctg ctctgcgtgc tttccacgac   540
168  gaacacggta tccgtaccga atcttggtct ccgctggctc gtcgttctga actgctgacc   600
170  gaacagctgc tgcaggaact ggctgttgtt tacggtgtta ccccgaccca ggttgttctg   660
172  cgttggcacg ttcagctggg ttctacccccg atcccgaaat ctgctgaccc ggaccgtcag   720
174  cgtgaaaacg cagacgtttt cggtttcgct ctgaccgctg accaggttga cgctatctct   780
176  ggtctggaac gtggtcgtct gtgggacggt gacccggaca cccacgaaga aatgtagaag   840
178  ctt                                                                   843
181  <210> SEQ ID NO: 5
182  <211> LENGTH: 277
183  <212> TYPE: PRT
184  <213> ORGANISM: Corynebacterium species
186  <400> SEQUENCE: 5
188  Met Thr Val Pro Ser Ile Val Leu Asn Asp Gly Asn Ser Ile Pro Gln
189  1               5                   10                  15
191  Leu Gly Tyr Gly Val Phe Lys Val Pro Pro Ala Asp Thr Gln Arg Ala
192              20                  25                  30
194  Val Glu Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala
195          35                  40                  45
197  Ile Tyr Gly Asn Glu Glu Gly Val Gly Ala Ala Ile Ala Ala Ser Gly
198      50                  55                  60
200  Ile Ala Arg Asp Asp Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg
201  65                  70                  75                  80
203  His Asp Gly Asp Glu Pro Ala Ala Ala Ile Ala Glu Ser Leu Ala Lys
204              85                  90                  95
206  Leu Ala Leu Asp Gln Val Asp Leu Tyr Leu Val His Trp Pro Thr Pro
207              100                 105                 110
209  Ala Ala Asp Asn Tyr Val His Ala Trp Glu Lys Met Ile Glu Leu Arg
210          115                 120                 125
212  Ala Ala Gly Leu Thr Arg Ser Ile Gly Val Ser Asn His Leu Val Pro
213      130                 135                 140
215  His Leu Glu Arg Ile Val Ala Ala Thr Gly Val Val Pro Ala Val Asn
216  145                 150                 155                 160
218  Gln Glu Leu His Pro Ala Tyr Gln Gln Arg Glu Ile Thr Asp Trp Ala
219              165                 170                 175
221  Ala Ala His Asp Val Lys Ile Glu Ser Trp Gly Pro Leu Gly Gln Gly
222              180                 185                 190
224  Lys Tyr Asp Leu Phe Gly Ala Glu Pro Val Thr Ala Ala Ala Ala Ala
225              195                 200                 205
227  Ala Ala Leu Leu Thr Pro Ala Gln Ala Val Leu Arg Trp His Leu Gln Lys
228      210                 215                 220
230  Gly Phe Val Val Phe Pro Lys Ser Val Arg Arg Glu Arg Leu Glu Glu
231  225                 230                 235                 240
233  Asp Leu Asp Val Phe Asp Phe Asp Leu Thr Asp Thr Glu Ile Ala Ala
234              245                 250                 255
236  Ile Asp Ala Met Asp Pro Gly Asp Gly Ser Gly Arg Val Ser Ala His
237              260                 265                 270
239  Pro Asp Glu Val Asp
```

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```
240           275
242 <210> SEQ ID NO: 6
243 <211> LENGTH: 277
244 <212> TYPE: PRT
245 <213> ORGANISM: Corynebacterium species
247 <400> SEQUENCE: 6
249 Met Pro Asn Ile Pro Thr Ile Ser Leu Asn Asp Gly Arg Pro Phe Pro
250 1               5                   10                  15
252 Glu Leu Gly Leu Gly Thr Tyr Asn Leu Arg Gly Asp Glu Gly Val Ala
253             20                  25                  30
255 Ala Met Val Ala Ala Ile Asp Ser Gly Tyr Arg Leu Leu Asp Thr Ala
256         35                  40                  45
258 Val Asn Tyr Glu Asn Glu Ser Glu Val Gly Arg Ala Val Arg Ala Ser
259         50                  55                  60
261 Ser Val Asp Arg Asp Glu Leu Ile Val Ala Ser Lys Ile Pro Gly Arg
262 65                  70                  75                  80
264 Gln His Gly Arg Ala Glu Ala Val Asp Ser Ile Arg Gly Ser Leu Asp
265                 85                  90                  95
267 Arg Leu Gly Leu Asp Val Ile Asp Leu Gln Leu Ile His Trp Pro Asn
268             100                 105                 110
270 Pro Ser Val Gly Arg Trp Leu Asp Thr Trp Arg Gly Met Ile Asp Ala
271             115                 120                 125
273 Arg Glu Ala Gly Leu Val Arg Ser Ile Gly Val Ser Asn Phe Thr Glu
274         130                 135                 140
276 Pro Met Leu Lys Thr Leu Ile Asp Glu Thr Gly Val Thr Pro Ala Val
277 145                 150                 155                 160
279 Asn Gln Val Glu Leu His Pro Tyr Phe Pro Gln Ala Ala Leu Arg Ala
280             165                 170                 175
282 Phe His Asp Glu His Gly Ile Arg Thr Glu Ser Trp Ser Pro Leu Ala
283             180                 185                 190
285 Arg Arg Ser Glu Leu Leu Thr Glu Gln Leu Leu Gln Glu Leu Ala Val
286         195                 200                 205
288 Val Tyr Gly Val Thr Pro Thr Gln Val Val Leu Arg Trp His Val Gln
289         210                 215                 220
291 Leu Gly Ser Thr Pro Ile Pro Lys Ser Ala Asp Pro Asp Arg Gln Arg
292 225                 230                 235                 240
294 Glu Asn Ala Asp Val Phe Gly Phe Ala Leu Thr Ala Asp Gln Val Asp
295                 245                 250                 255
297 Ala Ile Ser Gly Leu Glu Asn Gly Arg Leu Trp Asp Gly Asp Pro Asp
298                 260                 265                 270
    Thr Phe Gly Leu Met Ala
301             275
```

**VERIFICATION SUMMARY**                    DATE: 01/19/2002
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```
L:11  M:270 C: Current Application Number differs, Replaced Current Application No
L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:30  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:58  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:58  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:109 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:113 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:139 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:141 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
```